

Exploring metabolic pathways in genome-scale networks via generating flux modes.

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Abstract

The reconstruction of metabolic networks at the genome scale has allowed the analysis of metabolic pathways at an unprecedented level of complexity. Elementary flux modes (EFMs) are an appropriate concept for such analysis. However, their number grows in a combinatorial fashion as the size of the metabolic network increases, which renders the application of EFMs approach to large metabolic networks difficult. Novel methods are expected to deal with such complexity.

Involved units

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